

GenCore Version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:38:41; Search time 26.8605 Seconds

(Without alignments)  
843.812 Million cell updates/sec

Title: US-09-622-613B-15  
Perfect score: 602  
Sequence: 1 ONMATFOOKHIIWPIICNT.....ICVACENQYPVHFGICRCP 110

Scoring table: BIOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database:

1: SPREMBL\_21:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_protist:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_rvirus:\*

16: sp\_bacteriap:\*

17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	591.5	38.3	133	13	Q9PWR7 rana catesb
2	560.5	33.1	133	13	Q9SMO rana catesb
3	487.5	31.0	133	13	Q9SM2 rana catesb
4	478.5	79.5	133	13	Q9SM9 rana catesb
5	471.5	78.3	133	13	Q9SM8 rana catesb
6	448.5	74.5	133	13	Q9SM1 rana catesb
7	376	62.5	132	13	Q9DF8 rana catesb
8	281.5	46.8	127	13	Q918V rana catesb
9	277.5	46.1	127	13	Q8UVX rana pipien
10	246	40.9	129	13	Q9DF6 rana catesb
11	229.5	38.1	128	13	Q9DF8 rana catesb
12	226.5	37.6	128	13	Q9DF7 rana catesb
13	217.5	36.1	128	13	Q9DF5 rana catesb
14	163	27.1	169	13	Q9W73 xenopus lae
15	131	21.8	170	6	Q9BEC1
16	126	20.9	150	11	Q8VD94 beryllus ja

17	125.5	20.8	163	6	Q9BDC2	Q9bdc2 antilocapra
18	124.5	20.7	116	6	Q9TVC0	Q9tvc0 sus scrofa
19	124	20.6	150	11	Q8VD88	Q8vd88 rattus norv
20	122.5	20.3	144	6	Q9BH14	Q9bh14 antilocapra
21	120	19.9	150	11	Q8VD92	Q8vd92 rattus exul
22	116.5	19.4	152	11	Q8VD89	Q8vd89 rattus norv
23	115.5	19.2	119	6	Q9TV33	Q9tv33 bos taurus
24	114.5	19.0	124	6	Q95NE6	Q95ne6 bubalus bub
25	112.5	18.7	149	11	Q8VD95	Q8vd95 beryllus bo
26	112	18.6	134	6	Q9BD99	Q9bd99 tragulus ja
27	111.5	18.5	152	11	Q8VD84	Q8vd84 rattus tior
28	111.5	18.5	156	6	Q8SQ05	Q8sq05 jagochrix i
29	110.5	18.4	119	6	Q9TV30	Q9tv30 saguinus oe
30	110.5	18.4	119	6	Q9TV32	Q9tv28 eulemur ful
31	110.5	18.4	124	6	Q9TSF2	Q9tsf2 bos taurus
32	109.5	18.2	142	6	Q9BEC3	Q9bec3 tragulus ja
33	109.5	18.2	156	6	Q8SQ06	Q8sq06 ateles geof
34	109	18.1	124	6	Q9BEC2	Q9bec2 tragulus ja
35	108.5	18.0	156	6	Q8SQ08	Q8sq08 salmuri scl
36	108.5	18.0	156	6	Q8SQ07	Q8sq07 saguinus oe
37	107.5	17.9	152	11	Q8VD90	Q8vd90 rattus fusc
38	106.5	17.7	116	6	Q97933	Q97933 phocoenode
39	106.5	17.7	149	11	Q8VD93	Q8vd93 rattus exul
40	105.5	17.5	116	6	Q97934	Q97934 pseudorca c
41	105.5	17.5	119	6	Q9TSQ6	Q9tsq6 cercopithec
42	104.5	17.4	119	6	Q9TV32	Q9tv32 gorilla gor
43	104.5	17.4	124	6	Q9XS40	Q9xs40 camelus bac
44	104	17.3	158	6	Q8SPY2	Q8spy2 callithrix
45	103.5	17.2	158	6	Q8SPY3	Q8spy3 saguinus la

## ALIGNMENTS

RESULT 1

Q9PWR7 ID Q9PWR7 PRELIMINARY: PRT: 133 AA.

AC Q9PWR7:

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Ribonuclease precursor.

GN RCR.

OS Rana catesbeiana (Bull frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.

OX NCBI\_TaxID=8400;

RM [1]

RP SEQUENCE FROM N.A.

RC TISSUE=LIVER;

RX MEDLINE=98165825; PubMed=9497370;

RA Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;

RT "The Rana catesbeiana for gene encoding a cytochrome ribonuclease.

RT Tissue distribution, cloning, purification, cytotoxicity, and active

RT residues for RNase activity."

RL J. Biol. Chem. 273:6395-6401(1998).

DR EMBL: AF039104; AAD10702.1;

DR HSSP: P11916; IBC4.

DR InterPro: IPR001427; RNaseA.

DR Pfam: PF00074; RNaseA; 1.

DR Prodom: PD000535; RNaseA; 1.

DR SMART: SM00092; RNase\_Pc; 1.

DR PROSITE: PS00127; RNASE\_PANCREATIC; UNKNOWN\_1.

KW SIGNAL.

FT SIGNAL 1 22 POTENTIAL.

FT CHAIN 23 133 RIBONUCLEASE.

FT SIGNAL 133

SO SEQUENCE 133 AA; 14762 MW; A7D62594F7D16F0C CRC64;

Query Match Score 591.5; DB 13; Length 133;

Best Local Similarity 99.1%; Pred. No. 6.5e-61;

Matches 110; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ONMATFOOKHIIWPIICNT...CNTIMDNINIVGGCKRVNFTTISATVKAICTGVINMNV 59

DB 23 QNMATFOQKHIIINTPII-CNTIMDNIIYVGGCKRVNTFISSATVKAICGVINMV 82  
 OY 60 LSTRFOLNCTRTSITPRPCPYSSRTETNYICVKCENQVPHFAGIGRCP 110  
 DB 83 LSTRFOLNCTRTSITPRPCPYSSRTETNYICVKCENQVPHFAGIGRCP 133

## RESULT 2

O98SMO PRELIMINARY: PRT: 133 AA.

AC O98SMO: 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 OS RNAse A-type ribonuclease rc208 precursor.  
 CC Rana catesbeiana (Bull frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA MEDLINE=21539506; PubMed=11683320;  
 RT "Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;  
 RT "Rapid diversification of RNAse A superfamily ribonuclease from the  
 RT bullfrog, Rana catesbeiana.";  
 RL J. Mol. Evol. 53:31-38(2001).  
 DR EMBL: AF351209; AAK30255.1;  
 DR HSSP: P11916; 1BC4.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; rnaasea; 1.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; UNKNOWN\_1.  
 KW Signal.  
 FT SIGNAL.  
 SQ SEQUENCE 133 AA; 14628 MW; 87FCF122C349E02 CRC64;

Query Match 93.1%; Score 560.5; DB 13; Length 133;  
 Best Local Similarity 94.6%; Pred. No. 2, 6e-57;  
 Matches 105; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

OY 1 QNMATFOQKHIIINTPII-CNTIMDNIIYVGGCKRVNTFISSATVKAICGVINMV 59  
 DB 23 QNMATFOQKHIIINTPII-CNTIMDNIIYVGGCKRVNTFISSATVKAICGVINMV 82  
 OY 60 LSTRFOLNCTRTSITPRPCPYSSRTETNYICVKCENQVPHFAGIGRCP 110  
 DB 83 LSTRFOLNCTRTSITPRPCPYSSRTETNYICVKCENQVPHFAGIGRCP 133

## RESULT 3

O98SMO PRELIMINARY: PRT: 132 AA.

AC O98SMO: 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 OS RNAse A-type ribonuclease rc203 precursor (RC-RNase7 precursor).  
 CC Rana catesbeiana (Bull frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA MEDLINE=21539506; PubMed=11683320;  
 RT "Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;  
 RT "Rapid diversification of RNAse A superfamily ribonuclease from the  
 RT bullfrog, Rana catesbeiana.";  
 RL J. Mol. Evol. 53:31-38(2001).  
 DR EMBL: AF351210; AAK30256.1;  
 DR HSSP: P11916; 1BC4.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; rnaasea; 1.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; UNKNOWN\_1.  
 KW Signal.  
 FT SIGNAL.  
 SQ SEQUENCE 133 AA; 14615 MW; C8785B236B2654E CRC64;

Query Match 79.5%; Score 478.5; DB 13; Length 133;  
 Best Local Similarity 78.4%; Pred. No. 8, 4e-48;  
 Matches 87; Conservative 11; Mismatches 12; Indels 1; Gaps 1;

RA Liao Y.-D., Tang P.-C., Jeng J.-T.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF351207; AAK30253.1;  
 DR EMBL: AF359578; AAL87036.1;  
 DR HSSP: P11916; 1BC4.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; rnaasea; 1.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; UNKNOWN\_1.  
 KW Signal.  
 FT SIGNAL.  
 SQ SEQUENCE 132 AA; 14412 MW; 131A745187978687 CRC64;

Query Match 81.0%; Score 487.5; DB 13; Length 132;  
 Best Local Similarity 83.6%; Pred. No. 7, 5e-49;  
 Matches 92; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

OY 1 QNMATFOQKHIIINTPII-CNTIMDNIIYVGGCKRVNTFISSATVKAICGVINMV 59  
 DB 23 QNMATFOQKHIIINTPII-CNTIMDNIIYVGGCKRVNTFISSATVKAICGVINMV 82  
 OY 60 LSTRFOLNCTRTSITPRPCPYSSRTETNYICVKCENQVPHFAGIGRCP 109  
 DB 83 LSTRFOLNCTRTSITPRPCPYSSRTETNYICVKCENQVPHFAGIGRCP 132

## RESULT 4

O98SL9 PRELIMINARY: PRT: 133 AA.

AC O98SL9: 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 OS RNAse A-type ribonuclease rc212 precursor.  
 CC Rana catesbeiana (Bull frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA MEDLINE=21539506; PubMed=11683320;  
 RT "Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;  
 RT "Rapid diversification of RNAse A superfamily ribonuclease from the  
 RT bullfrog, Rana catesbeiana.";  
 RL J. Mol. Evol. 53:31-38(2001).  
 DR EMBL: AF351210; AAK30256.1;  
 DR HSSP: P11916; 1BC4.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; rnaasea; 1.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; UNKNOWN\_1.  
 KW Signal.  
 FT SIGNAL.  
 SQ SEQUENCE 133 AA; 14615 MW; C8785B236B2654E CRC64;

Query Match 79.5%; Score 478.5; DB 13; Length 133;  
 Best Local Similarity 78.4%; Pred. No. 8, 4e-48;  
 Matches 87; Conservative 11; Mismatches 12; Indels 1; Gaps 1;

OY 1 QNMATFOQKHIIINTPII-CNTIMDNIIYVGGCKRVNTFISSATVKAICGVINMV 59  
 DB 23 QNMATFOQKHIIINTPII-CNTIMDNIIYVGGCKRVNTFISSATVKAICGVINMV 82  
 OY 60 LSTRFOLNCTRTSITPRPCPYSSRTETNYICVKCENQVPHFAGIGRCP 110  
 DB 83 LSTRFOLNCTRTSITPRPCPYSSRTETNYICVKCENQVPHFAGIGRCP 133

## RESULT 5

O98SL8



[1]  
RN SEQUENCE FROM N.A.  
RP TISSUE=LIVER:  
RC MEDLINE=20330357; PubMed=10871370;  
RA "Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.:  
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a  
RT 3' UTR of unusual length and structure."  
RL Nucleic Acids Res. 28:2375-2382(2000).  
DR EMBL: AF165133; AAF76935.1;  
DR HSSP: P22069; IONC.  
DR InterPro: IPR001427; Rnasea.  
DR Pfam: PF00074; Rnasea; 1.  
DR ProDom: PD000535; Rnasea; 1.  
DR SMART: SM00092; Rnase\_Pc; 1.  
DR PROSITE: PS00127; Rnase\_PANCREATIC; UNKNOWN\_1.  
KW Signal.  
FT SIGNAL.  
SQ SEQUENCE 127 AA: 14491 MW: 8511DC5407AB65B CRC64;  
Query Match 46.8%; Score 281.5; DB 13; Length 127;  
Best Local Similarity 49.5%; Pred. No. 5.7e-25;  
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNATFOQKHINT-PIICNTIMDNNTIYVGQCKRVNTFISSATVKAICTGVI-NMN 58  
DB 24 QDWLTFQKHILTRDVCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIASKN 79  
59 VLSTTRQOLNCTRTSITPRCPYSSRTETNYICVGCENOPVPHFAGIGRC 109  
DB 80 VLTTSEVYLSDC---NVTSRPCKYKLLKKSNTKFCVTCENQAPVHFVGVGIC 127

RESULT 9  
Q8UVX5 PRELIMINARY; PRT; 127 AA.  
ID Q8UVX5  
AC Q8UVX5  
DT 01-MAR-2002 (TREMBlrel. 20, Created)  
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Oncogene precursor.  
GN RPR.  
OS Rana pipiens (Northern leopard frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
OX NCBI\_TaxID=8404;  
RN [1]  
RA Liao Y.-D., Wang S.-C.:  
RT "Rana pipiens onconase genomic DNA."  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF332139; AAL54383.1;  
DR InterPro: IPR001427; Rnasea.  
DR Pfam: PF00074; Rnasea; 1.  
DR ProDom: PD000535; Rnasea; 1.  
DR SMART: SM00092; Rnase\_Pc; 1.  
DR PROSITE: PS00127; Rnase\_PANCREATIC; UNKNOWN\_1.  
KW Signal.  
FT SIGNAL.  
SQ SEQUENCE 127 AA: 14469 MW: 953F90D351CFEE3 CRC64;  
Query Match 46.1%; Score 277.5; DB 13; Length 127;  
Best Local Similarity 49.5%; Pred. No. 1.6e-24;  
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNATFOQKHINT-PIICNTIMDNNTIYVGQCKRVNTFISSATVKAICTGVI-NMN 58  
DB 24 QDWLTFQKHILTRDVCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIASKN 79  
59 VLSTTRQOLNCTRTSITPRCPYSSRTETNYICVGCENOPVPHFAGIGRC 109  
DB 80 VLTTSEVYLSDC---NVTSRPCKYKLLKKSNTKFCVTCENQAPVHFVGVGIC 127

RESULT 10  
Q9DFY6 PRELIMINARY; PRT; 129 AA.  
ID Q9DFY6  
AC Q9DFY6  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE RC-Rnase2 ribonuclease precursor.  
OS Rana catesbeiana (Bull frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
OX NCBI\_TaxID=8400;  
RN [1]  
RA SEQUENCE FROM N.A.  
RP TISSUE=LIVER:  
RC MEDLINE=20512555; PubMed=11058105;  
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.:  
RT "Purification and cloning of cytotoxic ribonucleases from Rana  
RT catesbeiana (bullfrog)."  
RL Nucleic Acids Res. 28:4097-4104(2000).  
[2]  
RN SEQUENCE FROM N.A.  
RC TISSUE=LIVER:  
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.:  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF242555; AAC31441.2;  
DR HSSP: P22069; IONC.  
DR InterPro: IPR001427; Rnasea.  
DR Pfam: PF00074; Rnasea; 1.  
DR ProDom: PD000535; Rnasea; 1.  
DR SMART: SM00092; Rnase\_Pc; 1.  
DR PROSITE: PS00127; Rnase\_PANCREATIC; UNKNOWN\_1.  
KW Signal.  
FT SIGNAL.  
FT CHAIN 1 23 POTENTIAL.  
FT CHAIN 24 129 RC-RNASE2 RIBONUCLEASE.  
SQ SEQUENCE 129 AA: 14724 MW: 826A62862B10ABDA CRC64;  
Query Match 40.9%; Score 246; DB 13; Length 129;  
Best Local Similarity 43.4%; Pred. No. 7.5e-21;  
Matches 49; Conservative 24; Mismatches 30; Indels 10; Gaps 5;

QY 1 QNATFOQKHINT-PIICNTIMDNNTIYVGQCKRVNTFISSATVKAICTGVI-NMN 58  
DB 24 QDWLTFQKHILTRDVCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKRGVIRSAD 79  
59 VLSTTRQOLNCTRTSITPR-PCYSSRTETNYICVGCENOPVPHFAGIGRC 110  
DB 80 VLSNSEVYLAEC---NVKPRPCKYKLLKKSNTKFCVTCENQAPVHFVGVGICP 129  
RESULT 11  
Q9DFY8 PRELIMINARY; PRT; 128 AA.  
ID Q9DFY8  
AC Q9DFY8  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE RC-Rnase2 ribonuclease precursor.  
OS Rana catesbeiana (Bull frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
OX NCBI\_TaxID=8400;  
RN [1]  
RA SEQUENCE FROM N.A.  
RP TISSUE=LIVER:  
RC MEDLINE=20512555; PubMed=11058105;  
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.:  
RT "Purification and cloning of cytotoxic ribonucleases from Rana  
RT catesbeiana (bullfrog)."  
RL Nucleic Acids Res. 28:4097-4104(2000).  
[2]  
RN SEQUENCE FROM N.A.  
RC TISSUE=LIVER:

RA Liao Y.-D., Huang H.-C., Liew Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;  
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF242553; AAC31439.1;  
 DR HSSP: P22069; 10NC;  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; rnaasea.1.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; UNKNOWN\_1.  
 KM Signal.  
 FT SIGNAL.  
 FT CHAIN 1 23 POTENTIAL.  
 FT CHAIN 24 128 RC-RNASE2 RIBONUCLEASE.  
 SQ SEQUENCE 128 AA: 14839 MW: 989719CF52053ECC CRC64;  
 Query Match 38.1%; Score 229.5; DB 13; Length 128;  
 Best Local Similarity 40.2%; Pred. No. 6.1e-19;  
 Matches 45; Conservative 20; Mismatches 38; Indels 9; Gaps 4;  
 QY 1 QNNATFOQKHINT-PIICNTIMDNIIYVGQCKRYNFTIISATVKAICGV-1NM 58  
 Db 24 QNNATFOQKHINT-PIICNTIMDNIIYVGQCKRYNFTIISATVKAICGV-1NM 58  
 59 VLTSTFQNTCTRTSTTPRCPCYSSRTETNYICVCKENQYPVHAGIGRCP 110  
 Db 80 VLTSTFQNTCTRTSTTPRCPCYSSRTETNYICVCKENQYPVHAGIGRCP 110  
 RESULT 12  
 Q9DFY7 PRELIMINARY; PRT; 128 AA.  
 AC Q9DFY7;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE RC-RNase3 ribonuclease precursor.  
 OS Rana catesbeiana (bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.  
 OX NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LIVER;  
 RX MEDLINE=20512555; PubMed=11058105;  
 RA Liao Y.-D., Huang H.-C., Liew Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;  
 RT "Purification and cloning of cytotoxic ribonucleases from Rana  
 catesbeiana (bullfrog).";  
 RL Nucleic Acids Res. 28:4097-4104(2000).  
 DR EMBL: AF242553; AAC31440.2;  
 DR HSSP: P22069; 10NC;  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; rnaasea.1.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; UNKNOWN\_1.  
 KM Signal.  
 FT SIGNAL.  
 FT CHAIN 1 23 POTENTIAL.  
 FT CHAIN 24 128 RC-RNASE3 RIBONUCLEASE.  
 SQ SEQUENCE 123 AA: 14517 MW: 2B14986082E0587D CRC64;  
 Query Match 37.6%; Score 226.5; DB 13; Length 128;  
 Best Local Similarity 41.1%; Pred. No. 1.4e-18;  
 Matches 46; Conservative 18; Mismatches 39; Indels 9; Gaps 4;  
 QY 1 QNNATFOQKHINT-PIICNTIMDNIIYVGQCKRYNFTIISATVKAICGV-1NM 58  
 Db 24 QNNATFOQKHINT-PIICNTIMDNIIYVGQCKRYNFTIISATVKAICGV-1NM 58  
 59 VLTSTFQNTCTRTSTTPRCPCYSSRTETNYICVCKENQYPVHAGIGRCP 110  
 Db 80 VLTSTFQNTCTRTSTTPRCPCYSSRTETNYICVCKENQYPVHAGIGRCP 110  
 RESULT 13

Q9DFY5 PRELIMINARY; PRT; 128 AA.  
 AC Q9DFY5;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE RC-RNase6 ribonuclease precursor.  
 OS Rana catesbeiana (bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.  
 OX NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LIVER;  
 RX MEDLINE=20512555; PubMed=11058105;  
 RA Liao Y.-D., Huang H.-C., Liew Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;  
 RT "Purification and cloning of cytotoxic ribonucleases from Rana  
 catesbeiana (bullfrog).";  
 RL Nucleic Acids Res. 28:4097-4104(2000).  
 DR EMBL: AF242556; AAC31442.2;  
 DR HSSP: P22069; 10NC;  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; rnaasea.1.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; UNKNOWN\_1.  
 KM Signal.  
 FT SIGNAL.  
 FT CHAIN 1 23 POTENTIAL.  
 FT CHAIN 24 128 RC-RNASE6 RIBONUCLEASE.  
 SQ SEQUENCE 128 AA: 14804 MW: AFE8BD67D266C7C2 CRC64;  
 Query Match 36.1%; Score 217.5; DB 13; Length 128;  
 Best Local Similarity 39.3%; Pred. No. 1.5e-17;  
 Matches 44; Conservative 19; Mismatches 40; Indels 9; Gaps 4;  
 QY 1 QNNATFOQKHINT-PIICNTIMDNIIYVGQCKRYNFTIISATVKAICGV-1NM 58  
 Db 24 QNNATFOQKHINT-PIICNTIMDNIIYVGQCKRYNFTIISATVKAICGV-1NM 58  
 59 VLTSTFQNTCTRTSTTPRCPCYSSRTETNYICVCKENQYPVHAGIGRCP 110  
 Db 80 VLTSTFQNTCTRTSTTPRCPCYSSRTETNYICVCKENQYPVHAGIGRCP 110  
 RESULT 14  
 Q9W738 PRELIMINARY; PRT; 169 AA.  
 AC Q9W738;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE FRU2 protein.  
 GN FRU2.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
 OC Xenopodidae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96069863; PubMed=7585965;  
 RA Kinoshita N., Minshull J., Kirschner M.W.;  
 RT "The identification of two novel ligands of the fGF receptor by a  
 yeast screening method and their activity in Xenopus development.";  
 RL Cell 83:621-630(1995).  
 DR EMBL: AF061421; AAC31441.2;  
 DR HSSP: P22069; 10NC;  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; rnaasea.1.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; UNKNOWN\_1.  
 KM Signal.  
 FT SIGNAL.  
 FT CHAIN 1 23 POTENTIAL.  
 FT CHAIN 24 128 RC-RNASE6 RIBONUCLEASE.  
 SQ SEQUENCE 128 AA: 14804 MW: AFE8BD67D266C7C2 CRC64;  
 Query Match 36.1%; Score 217.5; DB 13; Length 128;  
 Best Local Similarity 39.3%; Pred. No. 1.5e-17;  
 Matches 44; Conservative 19; Mismatches 40; Indels 9; Gaps 4;  
 QY 1 QNNATFOQKHINT-PIICNTIMDNIIYVGQCKRYNFTIISATVKAICGV-1NM 58  
 Db 24 QNNATFOQKHINT-PIICNTIMDNIIYVGQCKRYNFTIISATVKAICGV-1NM 58  
 59 VLTSTFQNTCTRTSTTPRCPCYSSRTETNYICVCKENQYPVHAGIGRCP 110  
 Db 80 VLTSTFQNTCTRTSTTPRCPCYSSRTETNYICVCKENQYPVHAGIGRCP 110  
 RESULT 15

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF159166; AAD41901.1; -  
 DR HSSP; P00656; IL5Q.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA; 1.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNase\_PANCREATIC; UNKNOWN\_1.  
 SQ SEQUENCE 169 AA; 18891 MW; D969FE43B3CE1B8 CRC64;

Query Match 27.1%; Score 163; DB 13; Length 169;  
 Best Local Similarity 39.3%; Pred. No. 4.3e-11;  
 Matches 44; Conservative 10; Mismatches 50; Indels 8; Gaps 6;

OY 1 QNNATFOQKHII--NTPILCN-TIMDNIIYVGGCKRVNTEFI-ISSATVYKAICTGVIN 56  
 DB 28 QNINAFMEKHIVGAGTNCNOTIKDNIRF-KNCKEFRNFIHDTNGKKVKEKAGIYK 86  
 OY 57 MN-VLSTTRFQNLCTRTSITPRP--CPYSSRTETNYICVKNQYVPHFAG 105  
 DB 87 STVVISKELLPLTDCLMGRTARPPNCAYNQTRTGVINITCENNYPVHFG 138

## RESULT 15

O9BEC1 PRELIMINARY; PRT; 170 AA.

ID O9BEC1  
 AC O9BEC1;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Brain-type ribonuclease ribonuclease precursor (Fragment).  
 GN RNASE B.  
 OS Tragus javanicus (lesser Malay chevrolain).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Tragulina;  
 OC Tragulidae; Tragulus.  
 OC NCBI\_TaxID-9849;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-21347458; PubMed-11453981;  
 RA Breukelman H.J., Jekel P.A., Dubois J.Y., Mulder P.P.M.F.A.,  
 RA Wamelis H.W., Belantema J.J.;  
 RT "Secretory ribonucleases in the primitive ruminant chevrolain  
 (Tragus javanicus).";  
 RT Eur. J. Biochem. 268:3890-3897(2001).  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 DR EMBL: AJ271299; CAC24723.1; -  
 DR HSSP; P00656; IL5Q.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA; 1.  
 DR PRINTS: PR00794; RIBONUCLEASE.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; 1.  
 KW Endonuclease; Hydrolase; Nuclease; Signal.  
 FT NON\_TER 1  
 FT SIGNAL 1  
 FT CHAIN 20 19 POTENTIAL.  
 FT CHAIN 20 170 BRAIN-TYPE RIBONUCLEASE RIBONUCLEASE.  
 SQ SEQUENCE 170 AA; 18832 MW; ABCE7E1E5549AA0 CRC64;

Query Match 21.8%; Score 131; DB 6; Length 170;  
 Best Local Similarity 33.1%; Pred. No. 2.2e-07;  
 Matches 41; Conservative 17; Mismatches 46; Indels 20; Gaps 7;

OY 4 ATFOQKHII-----INTPIICNTIMDNIIYVGGCKRVNTEFIISATVYKAICT-----52  
 DB 25 AKFRRLDAGNNSINSN-ICNLMMKRR-KWTHGRCKPVNTEFIHESLEDKAICSEKNIT 82  
 OY 53 ----GVIMMNVLSTTRFQNLCTRTSITPRP--CPYSSRTETNYICVKNQYVPHFAGI 106  
 DB 83 CKNGPNCNCHOSNRP-AMITDCROTGSGSKYPNCAYKTSOKOKYIIVACEGTSPVPHFDGS 141  
 OY 107 GRCP 110

DB 142 AVLP 145

Search completed: June 25, 2003, 14:55:18  
 Job time : 26.9438 secs